

## FIGURE 1

CTCTTTTGTCCACCAGCCCAGCCTGACTCCTGGAGATTGTGAATAGCTCCATCCAGCCTG  
AGAAACAAGCCGGGTGGCTGAGCCAGGCTGTGCACGGAGCACCTGACGGGCCCAACAGAC  
CC

><MET {trans=1-s, dir=f, res=1}

ATGCTGCATCCAGAGACCTCCCCTGGCCGGGGGCATCTCCTGGCTGTGCTCCTGGCCCTC  
CTTGGCACCACCTGGGCAGAGGTGTGGCCACCCCAGCTGCAGGAGCAGGCTCCGATGGCC  
GGAGCCCTGAACAGGAAGGAGAGTTTCTTGCTCCTCTCCCTGCACAACCGCCTGCGCAGC  
TGGGTCCAGCCCCCTGCGGCTGACATGCGGAGGCTGGACTGGAGTGACAGCCTGGCCCAA  
CTGGCTCAAGCCAGGGCAGCCCTCTGTGGAATCCCAACCCCGAGCCTGGCATCCGGCCTG  
TGGCGCACCCCTGCAAGTGGGCTGGAACATGCAGCTGCTGCCCGCGGGCTTGGCGTCTTTT  
GTTGAAGTGGTCAGCCTATGGTTTGCAGAGGGGGCAGCGGTACAGCCACGCGGCAGGAGAG  
TGTGCTCGCAACGCCACCTGCACCCACTACACGCAGCTCGTGTGGGCCACCTCAAGCCAG  
CTGGGCTGTGGGCGGCACCTGTGCTCTGCAGGCCAGACAGCGATAGAAGCCTTTGTCTGT  
GCCTACTCCCCCGGAGGCAACTGGGAGGTCAACGGGAAGACAATCATCCCCTATAAGAAG  
GGTGCCTGGTGTTCGCTCTGCACAGCCAGTGTCTCAGGCTGCTTCAAAGCCTGGGACCAT  
GCAGGGGGGCTCTGTGAGGTCCCCAGGAATCCTTGTCGCATGAGCTGCCAGAACCATGGA  
CGTCTCAACATCAGCACCTGCCACTGCCACTGTCCCCCTGGCTACACGGGCAGATACTGC  
CAAGTGAGGTGCAGCCTGCAGTGTGTGCACGGCCGGTTCCGGGAGGAGGAGTGCTCGTGC  
GTCTGTGACATCGGCTACGGGGGAGCCCAGTGTGCCACCAAGGTGCATTTTCCCTTCCAC  
ACCTGTGACCTGAGGATCGACGGAGACTGCTTCATGGTGTCTTCAGAGGCAGACACCTAT  
TACAGAGCCAGGATGAAATGTCAGAGGAAAGCGGGGTGCTGGCCCAGATCAAGAGCCAG  
AAAGTGACAGACATCCTCGCCTTCTATCTGGGCCCGCCTGGAGACCACCAACGAGGTGACT  
GACAGTGACTTCGAGACCAGGAACCTTCTGGATCGGGCTCACCTACAAGACCGCCAAGGAC  
TCCTTCCGCTGGGCCACAGGGGAGCACCAGGCCTTACCAGTTTTTGCCTTTGGGCAGCCT  
GACAACCACGGGCTGGTGTGGCTGAGTGTGCCATGGGGTTTGGCAACTGCGTGGAGCTG  
CAGGCTTCAGCTGCCTTCAACTGGAACGACCAGCGCTGCAAAACCCGAAACCGTTACATC  
TGCCAGTTTGGCCAGGAGCACATCTCCCGGTGGGGCCCAGGGTCCTGAGGCCTGACCACA  
TGGCTCCCTCGCCTGCCCTGGGAGCACCGGCTCTGCTTACCTGTCTGCCACCTGTCTGG  
ACAAGGGCCAGGTTAAGACCACATGCCTCATGTCCAAAGAGGTCTCAGACCTTGCACAA  
TGCCAGAAGTTGGGCAGAGAGAGGCAGGGAGGCCAGTGAGGGCCAGGGAGTGAGTGTTAG  
AGAAGCTGGGGCCCTTCGCCTGCTTTTGATTGGGAAGATGGGCTTCAATTAGATGGCGA  
AGGAGAGGACACCGCCAGTGGTCCAAAAGGCTGCTCTCTTCCACCTGGCCCAGACCCTG  
TGGGGCAGCGGAGCTTCCCTGTGGCATGAACCCACGGGGTATTAAATTATGAATCAGCT  
GAAAAAAAAAAAAA

# FIGURE 2

1 CTCTTTTGTG CACCAGCCCA GCCTGACTCC TGGAGATTGT GAATAGCTCC ATCCAGCCTG AGAAACAAGC CGGGTGGCTG AGCCAGGCTG TGCACGGAGC  
GAGAAAACAG GTGGTCGGGT CGGACTGAGG ACCTCTAACA CTATATCGAG TAGGTCGGAC TCTTTGTTTC GCCCACCGAC TCGGTCCGAC ACCTGCTCTG

101 ACCTGACGGG CCCAACAGAC CCATGCTGCA TCCAGAGACC TCCCTGGGCC GGGGGCATCT CCTGGCTGTG CTCCTGGCCC TCCTTGGCAC CACCTGGGCA  
TGGACTGCCG GGGTTGTCTG CGTACGACGT AGTCTCTCTG AGGGGACCGG CCCCCTAGTA GGACCGACAC GAGGACCGGG AGGAACCGTG GTGGACCGCT

1 M L H P E T S P G R G H L L A V L L A L L G T T W A  
\*MET

201 GAGGTGTGGC CACCCAGCT GCAGGAGCAG GCTCCGATGG CCGGAGCCCT GAACAGGAAG GAGAGTTTCT TGCTCTCTCT CCTGCACAAC CGCCTGCGCA  
CTCCACACCG GTGGGGTCGA CGTCTCTGTC CGAGGCTACC GGCCTCGGGA CTGTCTCTTC CTCTCAAAGA ACGAGGAGAG GGACGTGTGT GCGGACCGCT

27 E V R P P Q L Q E Q A P M A G A L N R K E S F L L L S L H N R L R S

301 GCTGGGTCCA GCGCCCTGCG GCTGACATGC GGAGGCTGGA CTGGAGTGGC AGCCTGGCCC AACTGGCTCA AGCCAGGGCA GCGCTCTGTG GAATCCCAAC  
CGACCCAGGT CCGGGGACGC CGTCTGTACG CCTCCGACCT GACCTCACTG TCGGACCGAG TTGAGCTCCG TCGGAGACAC CTTAGGGTTG

61 W V Q P P A A D M R R L D W S D S L A Q L A Q A R A A L C G I P T

401 CCGAGCCTG GCATCCGGCC TGTGGCGCAC CCTGCAAGTG GGCTGGAACA TGCAGTGTCT GCGCGCGGCG TTGGCGTCTT TTGTGAAGT GGTACGCTA  
GGGCTCGGAC CGTAGGCGCG ACACCGCGTG GGACGTTTAC CCGACCTTGT ACGTCGACGA CCGGCGCGCG AACCGCAGGA AACAACTTCA CCAGTCCGAT

94 P S L A S G L W R T L Q V G W N M Q L L P A G L A S F V E V V S L

501 TGGTTTGCAG AGGGGACCGG GTACAGCCAC GCGGCAGGAG AGTGTGCTCG CAACGCCACC TGCACCCACT ACACCGAGCT CGTGTGGGCC ACCTCAAGCC  
ACCAAACGTC TCCCGCTCGC CATGTCCGTTG CCGCGTCTCT TCACACGAGC GTTGGCGTGG ACGTGGGTGA TGTGGCTCGA GCACACCGCG TGGAGTTCGG

127 W F A E G Q R Y S H A A G E C A R N A T C T H Y T Q L V W A T S S Q

601 AGCTGGGCTG TGGGCGGCAC CTGTGCTCTG CAGGCCAGAC AGCGATAGAA GCCTTTGTCT GTGCCTACTC CCGCGGAGGC AACTGGGAGG TCAACGGGAA  
TCGACCCGAC ACCCGCGGTG GACACGAGAC GTCCCGTCTG TCGCTATCTT CCGAAACAGA CACGGATGAG GGGGCTCCG TTGACCTCTC AGTTGCCCTT

161 L G C G R H L C S A G Q T A I E A F V C A Y S P G G N W E V N G K

701 GACAATCATC CCCTATAAGA AGGGTGCTG GTGTTGCTC TGCACAGCCA GTGTCTCAGG CTGCTTCAAA GCCTGGGACC ATGCAGGGGG GCTCTGTGAG  
CTGTTAGTAG GGGATATCTT TCCACCGGAC CACAAGCGAG ACGTGTCCGT CACAGAGTCC GACGAAGTTT CCGACCTCGG TACGTCCCCC CGAGACACTC

194 T I I P Y K K G A W C S L C T A S V S G C F K A W D H A G G L C E

801 GTCCCCAGGA ATCCTTGTG CATGAGCTGC CAGAACCATG GACGTCTCAA CATCAGCACC TCCACTTGCC ACTGTCCCCC TGGCTACAGG GGCAGATACT  
CAGGGGTCTT TAGGAACAGC GTACTCGAGC GTCTTGTGAC CTGCAAGATT GTAGTGTGGG ACGGTGACGG TGACAGGGGG ACCGATGTGC CGGTCTATGA

227 V P R N P C R M S C Q N H G R L N I S T C H C H C P P G Y T R L R Y C

901 GCCAAGTGAG GTGCAGCCTG CAGTGTGTGC ACGGCGCGTT CCGGAGGAG GAGTGTCTGT GCGTCTGTGA CATCGGCTAC GGGGAGCGCC AGTGTGCCAC  
CGGTTCACTC CACGTCCGAC GTACACACAG TGCAGGCGAA GCGCTCTCTC CTCACAGGCA CGCAGACACT GTAGCCGATG CCGCTCCGGG TCACACGGTG

261 Q V R C S L Q C V H G R F R E E E C S C V C D I G Y G G A Q C A T

1001 CAAGGTGCAT TTTCCCTTCC ACACCTGTGA CCTGAGGATC GACGGAGACT GCTTCATGGT GTCTTCAGAG GCAGACACCT ATTACAGAGC CAGGATGAAA  
GTTCCACGTA AAAGGGGAAGG TGTGGCACTT GGACTCTTAG CTGCCTCTGA CGAAGTACCA CAGAAGTCTC CGTCTGTGGA TAATGTCTCG GTCCCTACTTT

294 K V H F P F H T C D L R I D G D C F M V S S E A D T Y Y R A R M K

1101 TGTACAGGGA AAGGCGGGGT GCTGGCCCGC ATCAAGAGCC AGAAAGTGCA GGACATCTCT GCCTTCTATC TGGGCGCGCT GGAGACACCC AACGAGGTGA  
ACAGTCTCTT TTCCGCCCCA CGACCGGGTC TAGTTCTCGG TCTTTACAGT CCTGTAGGAG CCGAAGTAG ACCCGCGGGA CTTCTGTGTG TTGCTCCACT

327 C Q R K G G V L A Q I K S Q K V Q D I L A F Y L G R L E T T N E V T

1201 CTGACAGTGA CTTGAGAGCC AGGAACCTCT GGATCCGGCT CACCTACAAG ACCGCCAAGG ACTCCTTCCG CTGGGCCACA GGGGAGCACC AGGCCTTCAC  
GACTGTCACT GAAGCTCTGG TCCTTGAAGA CCTAGCCCGA GTGGATGTTT TGGCGGTTCC TGAGGAAGGC GACCCGGTGT CCCCTCGTGG TCCGGAAGTG

361 D S D F E T R N F W I G L T Y K T A K D S F R W A T G E H Q A F T

1301 CAGTTTGTCC TTTGGGCAGC CTGACAACCA CCGGCTGGTG TGGCTGAGTG CTGCCATGGG GTTTGGCAAC TGGCTGGAGC TGCAGGCTTC AGCTGCTTTC  
GTCAAACCGG AAACCCGTCG GACTGTGGT GCGCGACCCAC ACCGACTCAC GACGGTACCC CAAACCGTTG ACGCACCTCG ACGTCCGAAG TCGACGGAAG

394 S F A F G Q P D N H G L V W L S A A M G F G N C V E L Q A S A A F

1401 AACTGGAACG ACCAGCGCTG CAAAACCCGA AACCGTTACA TCTGCCAGTT TGGCCAGGAG CACATCTCCC GGTGGGGCCC AGGGTCTCTA GGCCTGACCA  
TTGACCTTGC TGGTCGCGAC GTTTTGGGCT TTGGCAATGT AGACGGTCAA ACGGCTCCTC GTGTAGAGGG CCACCCCGGG TCCAGGACT CCGGACTGGT

427 N W N D Q R C K T R N R Y I C Q F A Q E H I S R W G P G S O

1501 CATGGCTCCC TCGCTGCCCC TGGGAGCACC GGCTCTGCTT ACCTGTCTGC CCACCTGTCT GGAACAAGGG CCAGGTAAAG ACCACATGCC TCATGTCCAA  
GTACCGAGGG AGCGGACGGG ACCCTCGTGG CCGAGACGAA TGGACAGAGC GGTGGACAGA CCTGTGTTCCC GGTCCAATTG TGGTGTACGG AGTACAGGTT

1601 AGAGGTCTCA GACCTTGCAC AATGCCAGAA GTTGGGCAGA GAGAGGCAGG GAGGCCAGTG AGGGCCAGGG AGTGAGTGTG AGAAGAAGCT GGGGCCCTTC  
TCTCCAGAGT CTGGAACGTG TTACGGTCTT CAACCCGTCT CTCTCCGTCC CTCCGGTCC TCCCGTCCC TCACTCACA TCTTCTTCGA CCGCGGGAAG

1701 GCCTGCTTTT GATTGGGAAG ATGGGCTTCA ATTAGATGGC GAAGGAGAGG ACACCGCCAG TGGTCCAAAA AGGCTGCTCT CTTCCACCTG GCCCAGACCC  
CGGACGAAAA CTAACCCCTC TACCCGAAGT TAATCTACCG CTCTCTCTCC TGTGGCGGTC ACCAGGTTTT TCCGACGAGA GAAGGTGGAC CCGGTCTGGG

1801 TGTGGGCGAG CCGAGCTTCC CTGTGGCATG AACCCACCGG GGTATTAAAT TATGAATCAG CTGAAAAAAA AAAAAA  
ACACCCCGTC GCCTCGAAGG GACACCGTAC TTGGGGTGCC CCATAATTTA ATACTTAGTC GACTTTTTTT TTTTTT

### **FIGURE 3**

><homology to cysteine-rich secretory proteins>

><signal peptide>

MLHPETSPGRGHLLAVLLALLGTTWA

><start mature protein>

EVWPPQLQEAPMAGALNRKESFLLLSLHNRLRSWVQPPAADMRRLDWSDSLAQLA  
QARAALCGIPTPSLASGLWRTLQVGWNMQLLPAGLASFVEVVSLWFAEGQRYSHAA  
GECAR

><potential N-glycosylation site>

NATCTHYTQLVWATSSQLGCGRHLCSAGQTAIEAFVCAYSPGGNWEVNGKTIIPYKK  
GAWCSLCTASVSGCFKAWDHAGGLCEVPRNPCRMSCQNHGRL

><potential N-glycosylation site>

NISTCH

><EGF-like domain cysteine pattern signature>

CHCPPGYTGRYCQVRCSLQCVHGRFREEECS

><EGF-like domain cysteine pattern signature>

CVCDIGYGGAQCATKVHFPFHTCDLRIDGDCFMVSSEADTYRARMKCQRKGGVLA  
QIKSQKVQDILAFYLGRLETTNEVTDSDFETRNFWIGLTYKTAKDSFRWATGEHQAF  
TSFAFGQPDNHGLVWLSAAMGFGN

><C-type lectin domain signature (CVELQASAAFNWNDQRCKTRNRYIC)>

CVELQASAAFNWNDQRCKTRNRYICQFAQEHISRWGPGS

## FIGURE 4

```

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44176
<subunit 1 of 1, 455 aa, 1 stop
<MW: 50478, pI: 8.44, NX(S/T): 2
< 1 10 20 30 40 50 60 70
< | | | | | | | | | | | | | |
MLHPETSPGRGHLLAVLLALLGTTWAEVWPPQLQEQA PMAGALNRKESFLLLSLHNRLRSWVQPPAADMR

< 71 80 90 100 110 120 130 140
< | | | | | | | | | | | | | |
RLDWSDSLQAQARAALCGIPTPSLASGLWRTLQVGWNMQLLPAGLASFVEVVS LWF AEGQRYSHAAGE

< 141 150 160 170 180 190 200 210
< | | | | | | | | | | | | | |
CARNATCTHYTQLVWATSSQLGCGRHLCSAGQTAIEAFVCAYSPGGNWEVNGKTIIPYKKGAWCSLCTAS

< 211 220 230 240 250 260 270 280
< | | | | | | | | | | | | | |
VSGCFKAWDHAGGLCEVPRNPCRMSQNHGRLLNISTCHCHCPPGYTG RY CQVRC SLQCVHGRFRREEECSC

< 281 290 300 310 320 330 340 350
< | | | | | | | | | | | | | |
VCDIGYGAQCATKVHFPFHTCDLRIDGDCFMVSSEADTYRARMK CQRKGGVLAQIKSQKVQDILAFYL

< 351 360 370 380 390 400 410 420
< | | | | | | | | | | | | | |
GRLETTNEVTDSDFE TRNFWIGLTYKTA KDSFRWATGEHQAF TSFAFGQPDNHGLVWLSAAMGFNCVEL

< 421 430 440 450
< | | | | | | | | | |
QASAAFNWNDQRC KTRNRYICQFAQEHISRWGPGS

```

### FIGURE 5A

2989336	1	GCTGGGAAGANGGCGCCAGAAAGGCAGCTGGCAGCAGACTCCAGGGTCTGA
W79362	1	ACAG
<consen01>	1	.... ACAG
2989336	51	GTGGGCCAACCTTGACTACNCCGGCCCCAGGGCTCACCTACAAGACCGCCA
W79362	5	TGACTTCGAGACCAGGAAC TTCTGGATCGGGCTCACCTACAAGACCGCCA .....+.+.....++...+.+.....+++++
<consen01>	5	TGACTTCGAGACCAGGAAC TTCTGGATCGGGCTCACCTACAAGACCGCCA
2989336	101	AGGACTCCTTCCGCTGGGCCACAGGGGAGCACCAGGCCTTCACCAGTTTT
W79362	55	AGGACTCCTTCCGCTGGGCCACAGGGGAGCACCAGGCCTTCACCAGTTTT +++++
<consen01>	55	AGGACTCCTTCCGCTGGGCCACAGGGGAGCACCAGGCCTTCACCAGTTTT
2989336	151	GCCTTTGGGCAGCCTGACAACCACGGGTTTGGCAACTGCGTGGAGCTGCA
W79362	105	GCCTTTTGN-AGCCTGACAACCACGGGTTTGGCAACTGCGTGGAGCTGCA
2554374	1	TGCGTGGAGCTGCA
<consen01>	105	+++++++ .+++++ GCCTTTGGGCAGCCTGACAACCACGGGTTTGGCAACTGCGTGGAGCTGCA
2989336	201	GG-TTCAGCTGCCTTCAACTGGAACAACCAGCG-TGCAAACCCGAAACC
W79362	154	GGCTTCAGCTGCCTTCAACTGGAACGACCAGCGCTGCAAACCCGAAACC
2554374	15	GGCTTCAGCTGCCTTCAACTGGAACGACCAGCGCTGCAAACCCGAAACC
2992967	1	AACC
<consen01>	155	+++++++ .+++++ GGCTTCAGCTGCCTTCAACTGGAACGACCAGCGCTGCAAACCCGAAACC
2989336	249	GTTACATCTGCCAGTTTGCCCAGGAGCACATCTCCCGGTGGGGNCAG
W79362	204	GTTACATCTGCCAGTTTGCCCAGGAGCACATCTCCCGGTGGGGCCCATGG
2554374	65	GTTACATCTGCCAGTTTGGTGAGGGA CTTCCTGAGGCTCCCCTTCTC-TG
2992967	5	GTTACATCTGCCAGTCTGCCCAGNGCACATCTCCCGGTGGGGCCCA-GG
2673172	1	GGCCCA-GG
<consen01>	205	+++++++ .++...+++.+ .....+.. .+ GTTACATCTGCCAGTTTGCCCAGGAGCACATCTCCCGGTGGGGCCCA GG
W79362	254	GTCCTGATGGCCTGACCACATGGCTCCCTCGCCTGCCCTGGGAGACCGG
2554374	114	ATCCCTG-ACCCTGGGGGTGCTGCTGACCCGGTCCAGCCTGCAAGGGTAT
2992967	54	GTCCTGA-GGCCTGACCACATGGCTCCCTCGCCTGCCCTGGGAGACCGG
2673172	9	GTCCTGA-GGCCTGACCACATGGCTCCCTCCCCTGCCCTGNGANCACCGG .+++... ..++++.....++...+.+.....+.....+.....
<consen01>	254	GTCCTGA GGCCTGACCACATGGCTCCCTCGCCTGCCCTGGGAGACCGG
W79362	304	CTCTGCTTACCTGTCTGCCCACCTNGTCTGNAACAAGGGCCAAGGTTAAG
2554374	163	CTAGGTGGCAGGTT CAGAGTGGGT-CTGGGCACACGGGGCCA-TAGAGGA
2992967	103	CTCTGCTTACCTGTCTGCCCACCT-GTCTGGAACAAGGGCCA-GGTTAAG
2673172	58	CTCTGCTTACCTGTCTGCCCACCT-GTCTGGAACAAGGGCCA-GGTTAAG ++.+. ....+++.+ .....+ .+.+.+ .....+ .....
<consen01>	303	CTCTGCTTACCTGTCTGCCCACCT GTCTGGAACAAGGGCCA GGTTAAG

**FIGURE 5B**

W79362	354	ATCACATGCCTCATGTCCAAAGAAGGTCCTCAGACTTTGCACAATGCCAGA
2554374	211	TGCCCTGTGTGATGGCCTTGTACC-TGTGGGCTCCTGAGCCCAGAG
2992967	151	ATCACATGCCTCATGTCCAAAGA-GGTCTCAGACCTTGCCACAATGCCAGA
2673172	106	ACCACATGCCTCATGTCCAAAGA-GGTCTCAGACCTTGCCACAATGCCAGA
AA527105	1	GGTCGACCTTGCCACAATGCCAGA
197200	1	ANTNCCAGA
<consen01>	351	..+..+.....+. .++.....+.++.+++++
		ATCACATGCCTCATGTCCAAAGA GGTCTCAGACCTTGCCACAATGCCAGA
W79362	404	AGTTGGGT
2992967	200	NGTTGGGCAGAGAGAGGCAGGGAGGCCAGTGAGGCC-AGG-AGTGAGTGT
2673172	155	AGTTGGGCAGAGAGAGGCAGGGAGGCCAGTGAGGGNNAGGGAGTGANTGT
AA527105	24	AGTTGGGCAGAGAGAGGCAGGGAGGCCAGTGAGGGCGAGGGAGTGAGTGT
197200	10	NGTTGGGCAGAGAGAGGCAGGGAGGCCAGTNAGGGCCAGGCAGTGAGTNT
<consen01>	400	.+++++.+++++.+++++.+++++.+++.. ++++.+++++.+.+
		AGTTGGGCAGAGAGAGGCAGGGAGGCCAGTGAGGGCGAGGGAGTGAGTGT
2992967	248	TAGAAGAAG-TGGGGN--TTCGNCTG-TTTTGNT-GGGA-G-TGGG-TTC
2673172	205	TAGAAGAAGCTGGGGTCCTTCGCCTGCTTTTGATTG
AA527105	74	TAGAAGAAGCTGGGGCCCTTCGCCTGCTTTTGATTGGGAAGATGGGCTTC
197200	60	TAGACGAAGCTGGGGCCCNCGCCTNCTTTTNATTNGNNAGATGGGCTNN
<consen01>	450	++++.+++++.++.+.+.+.+++++.+.+.+.+++++.+.+
		TAGAAGAAGCTGGGGCCCTTCGCCTGCTTTTGATTGGGAAGATGGGCTTC
2992967	290	A-TTAGATGGC
AA527105	124	AATTAGATGGCGAAGGAGAGGACACCGCCAGTGGTCCAAAAGGCTGCTC
197200	110	AATNAGATNGCGAAGGAGAGGACACCNCCANTGGTCCAAAAGGCT
2127437	1	GAGGACACCGCCAGTGGTCCAAAAGGCTGCTC
<consen01>	500	+++..++++.+++++.+++++.+++..+++++.+++++.++++.
		AATTAGATGGCGAAGGAGAGGACACCGCCAGTGGTCCAAAAGGCTGCTC
AA527105	174	TCTTCCACCTGGCCCAGACCCTGTGGG-CAGCGGACTTCCCTGTGGCATG
2127437	34	TCTTCCACCTGGCCCAGACCCTGTGGGGCAGCGGACTTCCCTGTGGCATN
<consen01>	550	+++++.+++++.+++++.+++++.+++++.+++++.+++++.++++.
		TCTTCCACCTGGCCCAGACCCTGTGGGGCAGCGGACTTCCCTGTGGCATG
AA527105	223	AACCCACGGGTAATTAAATTATGAATCAGCTGAAAGAAGAAAAAGTCGG
2127437	84	AACCCACGGGGTATTAAATTATGAATCAGCTG
<consen01>	600	+++++.+++++.+++++.+++++.+++++.+++++.+++++.++++.
		AACCCACGGGTAATTAAATTATGAATCAGCTGAAAGAAGAAAAAGTCGG
AA527105	273	CG
<consen01>	650	++ CG

## **FIGURE 6**

```
ACAGTGACTTCGAGACC
><39499.f1 {underline=1-24, dir=f}>
AGGAACTTCTGGATCGGGCTCACCTACAAGACC
><39499.p1 {underline=1-45, dir=f}>
GCCAAGGACTCCTTCCGCTGGGCCACAGGGGAGCACCAGGCCTTCACCAGTTTTGCCTTT
GGGCAGCCTGACAACCACGGGTTTGGCAACTGCGTGGAGCTGCAGGCTTCAGCTGCCTTC
AACTGGAACGACCAGCGCTGCAAAACCCGAAACCGTTACATCTGCCAGTTTGCCCAGGAG
CACATCTCCCGGTGGGGCCCAGGGTCCTGAGGCCTGACCACATGGCTCCCTCGCCTGCCC
TGGGAGCACCGGCTCTGCTTACCTGTCTGCCCACCTGTCTGGAACAAGGGCCAGGTTAAG
ATCACATGCCTCATGTCCAAAGAGGTCTCAGACCTTGCACAATGCCAGAAGTTGGGCAGA
GAGAGGCAGGGAGGCCAGTGAGGGCGAGGGAGTGAGTGTTAGAAGAAGCTGGGGCCCTTC
GCCTGCTTTTGGATTGGGAAGATGGGCTTCAATTAGATGGCGAAGGAGAGGACACCGCCAG
TGGTCCAAAAAGGCTGCTCTCTTCCACCTGGCCCAGACC
><39499.r1 {underline=1-24, dir=b}>
CTGTGGGGCAGCGGACTTCCCTGTGGCATGAACCCACGGGTAATTAAATTATGAATCAG
CTGAAAGAAGAAAAAGTCGGCG
```

# FIGURE 7

```

1  ACAGTACTT CGAGACCAGG AACTTCTGGA TCGGGCTCAC CTACAAGACC GCCAAGACT CCTTCCGCTG GGCCACAGGG GAGCACCAGG CCTTCACCAG
   TGTCACTGAA GCTCTGGTCC TTGAAGACCT AGCCCGAGTG GATGTTCTGG CCGTTCTTGA GGAAGCGGAC CCGGTGTCCC CTCGTGGTCC GGAAGTGGTC
   ^39499.fl
101 TTTTGGCCTTT GGGCAGCCTG ACAACCACGG GTTTGGCAAC TGGGTGGAGC TGCAGGCTTC AGCTGCCCTTC AACTGGGAAG ACCAGCGCTG CAAAACCCGA
   AAAACGGAAA CCCGTGGAC TGTGTGGTGC CAAACCGTTG ACGCACCTCG ACGTCCGAAG TCGACGGAAG TTGACCTTGC TGGTCGGAC GTTTTGGGCT
201 AACCGTTACA TCTGCCAGTT TGCCCCAGGAG CACATCTCCC GTTGGGGCCC AGGTTCTTGA GGCTTGACCA CATGGCTCCC TCGCCTGCCC TGGGAGCACC
   TTGGCAATGT AGACGGTCAA ACGGGTCTTC GTGTAGAGGG CCACCCCGGG TCCCAAGACT CCGGACTGGT GTACCGAGGG AGCGGACGGG ACCCTCGTGG
301 GGCTCTGCTT ACCTGTCTGC CCACCTGTCT GGAACAAGGG CCAGGTTAAG ATCACATGCC TCATGTCCAA AGAGGTCTCA GACCTTGCAC AATGCCAGAA
   CCGAGACGAA TGGACAGACG GGTGGACAGA CCTTGTCTCC GGTCCAATTC TAGTGTACGG AGTACAGGTT TCTCCAGAGT CTGGAACGTC TTACGGTCTT
401 GTTGGGCAGA GAGAGGCAGG GAGGCCAGTG AGGGCGAGGG AGTGAGTGT AGAAGAAGCT GGGGCCCTTC GCCTGCTTTT GATTGGGAAG ATGGGCTTCA
   CAACCGTCT CTCTCCGTCC CTCCGCTCAC TCCCGTCCC TCACTCACA TCTTCTCTGA CCCCAGGAAG CGGACGAAAA CTAACCCCTTC TACCCGAAGT
501 ATTAGATGGC GAAGGAGAGG ACACCGCCAG TGGTCCAAAA AGGCTGCTCT CTTCACCTG GCCCAGACCC TGTGGGCGAG CGGACTTCCC TGTGGCATGA
   TAATCTACCG CTTCTCTCTC TGTGGCGGTC ACCAGGTTT TCCGACGAGA GAAGTGGAC CCGGTCTGGG ACACCCCGTC GCCTGAAGGG ACACCGTACT
   ^39499.r1
601 ACCCCACGGG TAATTAAAT ATGAATCAGC TGAAGAAGA AAAAGTCGGC G
   TGGGTGCCC ATTAATTAA TACTTAGTCG ACTTCTTCT TTTTCAGCCG C

```



## FIGURE 8

```

>1 S68683 cysteine-rich secretory protein 3 precursor - human (245 aa)
Score = 235 (82.7 bits), Expect = 5.2e-18, P = 5.2e-18
Identities = 51/157 (32%), Positives = 78/157 (49%), at 273,42, Frame = +3

DNA44176 273 LLSLHNRLRSWVQPPAADMRRLDWSDSLALQAQARAALCGIPTPSILASGLWRTLQVGWNN
S68683 42 IVNKHNELRRRAVSPPARNMLKMEWNKEAANAQKWANQCNY-RHSNPKDRMTSLKCGENL

DNA44176 453 QLLPAGLASFEVVSLSLWFAEGQRYSHAAGECARNATCTHYTQLVWATSSQLGCGRHLCSA
S68683 101 YMSSAS-SSWSQAIQSWFDEYNDFDFGVGPKTPNAVVGHYTQVVWYSSYLVGCGNAYCPN

DNA44176 633 GQTAIEAFVCAYSPGGNWEVNGKTIIPYKKGAWCSLC
S68683 160 QKVLKYYYVCQYCPAGNWA--NRLYVPYEQGAPCASC

```

## FIGURE 9

>8 ECCRISP3\_1 cysteine-rich secretory protein-3 - Equus caballus (245 aa)  
 Score = 216 (76.0 bits), Expect = 5.8e-16, P = 5.8e-16  
 Identities = 71/242 (29%), Positives = 109/242 (45%), at 159,3, Frame = +3

```

DNA44176 159 LLAALLLGGTTWAEVWPPQLQEQAPMAGALNRKE-SFLLLSLHNRLRSWVQPPADMR
ECCRISP3_1 3 LLPVLL-FLAAVLLPFFPASGQDPGFAALSITKSEVQKEIVNKHNDLRRITVSPLASNMLK

DNA44176 336 LDWSDSLAQLAQARAALCGIPTPSLASGLWRTLQVGWMMQLLPAGLASFVEVVSLEWFAEG
ECCRISP3_1 62 MQWDSKTATNAQNWANKCLLQHSKAEDRAVGTMKCGENL-FMSSIPNSWSDAIQNWHDDEV

DNA44176 516 QRYSHAAGECARNATCTHYTQLVWATSSQLGCGRHLCSAGQTAIEAFVCAYSPPGGNWEVN
ECCRISP3_1 121 HDFKYGVPKTPNAVVGHTYQVVWYSSYRVGCGIAYCPKQGTLYYYVVCQYCPAGNY-VN

DNA44176 696 GKTIIPIYKKGAWCS-----LCTAS-----VSGCFKAWDHAGGLCEVPRNPCRMSC
ECCRISP3_1 180 -KINTPYEQGTPCARCPGNCNGLCTNSCEYEDLVSNCDLSLKKIAGCEHELLKENCKTTC

DNA44176 831 QNHGRL
ECCRISP3_1 239 QCENKI

```

## FIGURE 10

>12 S68684 cysteine-rich secretory protein 1 precursor - human (249 aa)  
 Score = 207 (72.9 bits), Expect = 5.4e-15, P = 5.4e-15  
 Identities = 63/214 (29%), Positives = 96/214 (44%), at 273,44, Frame = +3

```

DNA44176 273 LLSLHNRLRSWVQPPAADMRRLDMSDSLAAQAAALCGIPTPS-LASGLWRTLQVGWN
S68684    44 IVNIHNALRRRVVPPASNMLKMSWSEEAQNARIFSKYCDMTESNPLERRLPNTF-CGEN

DNA44176 450 MQLLPAGLASFVEVVSLLWFAEGQRYSHAAGECARN-ATCTHYTQLVWATSSQLGCGRHL
S68684   103 MHMTSYPV-SWSSVIGVWYSESTSPKHGEWTTDDDDITTDHYTQIVWATSYLIGCALASC

DNA44176 627 SAGQTAIEAFVCAYSPGGNWEVNGKTIIPYKKGAWCSLCTASVSGCFKAWDHAGGLCEVP
S68684   162 RQQGSPLYLVCHYCHEGN-DPETKNE-PYKTGVPCEACP---SNC-----EDKLCT--

DNA44176 807 RNPCRMSCQNHGRLNISTCHCHCPPGYTGRCQVRC
S68684   209 -NPC-IYDEYFDCDIQVHYLGCNHSSTILFCKATC

```